

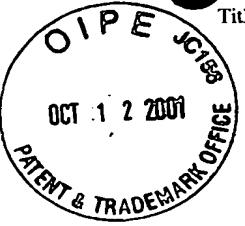
FIGURE 1A

Docket No.: PF-0181-2 CON

Inventors: Hillman et al.

Title: NOVEL HUMAN MEMBRANE PROTEIN

Serial No.: 09/898,216



5'	GGC	TTC	TGG	GAG	CNA	CCG	CTC	CGC	TGC	TCT	CGT	TGG	TTC	CGG	AGG	TCG	CTG	CGG	54
	9	18	27	36	45	54													
	63	72	81	90	99	108													
	CGG	TGG	GAA	ATG	CTG	GGC	GGC	GGG	GGG	CAC	TGG	GGG	CCT	TCT	GCT	GAG			
	M	L	A	R	A	A	R	G	H	W	G	P	F	A	E				
	117	126	135	144	153	162													
	GGG	CTC	TCT	ACT	GGC	TTC	TGG	CCG	CCG	TCC	GGC	GCC	TCC	TCT	GGA	TTC	CCC		
	G	L	S	T	G	F	W	P	R	S	G	R	A	S	S	G	L	P	
	171	180	189	198	207	216													
	CGA	AAC	ACC	GTG	GTG	GTA	CTG	TTC	GTG	CGG	CAG	GAG	GCC	TGG	GTG	GAG	CGA		
	R	N	T	V	V	L	F	V	P	Q	Q	E	A	W	V	V	E	R	
	225	234	243	252	261	270													
	ATG	GGC	CGA	TTC	CAC	CGG	ATC	CTG	GAG	CCT	GGT	TTG	AAC	ATC	CTC	ATC	CCT	GTG	
	M	G	R	F	H	R	I	L	E	P	G	L	N	I	L	I	P	V	
	279	288	297	306	315	324													
	TGA	GAC	CGG	ATC	CGA	TAT	GTG	CAG	AGT	CTC	AAG	GAA	ATT	GTC	ATC	AAC	GTG	CCT	
	L	D	R	I	R	Y	V	Q	S	L	K	E	I	V	I	N	V	P	
	333	342	351	360	369	378													
	GAG	CAG	TCG	GCT	GTG	ACT	CTC	GAC	AAT	GTA	ACT	CTG	CAA	ATC	GAT	GGA	GTC	CTT	
	E	Q	S	A	V	T	L	D	N	V	T	L	Q	I	D	G	V	L	

FIGURE 1A

387	TAC	CTG	CGC	ATC	ATG	GAC	CCT	TAC	AAG	GCA	AGC	TAC	GGT	GTG	GAG	GAC	CCT	GAG	432
Y	L	R	I	M	D	P	Y	K	A	S	Y	G	V	E	D	P	E		
441	TAT	GCC	GTC	ACC	CAG	CTA	GCT	CAA	ACA	ACC	ATG	AGA	TCA	GAG	CTC	GCC	AAA	CTC	486
Y	A	V	T	Q	L	A	Q	T	T	M	R	S	E	L	G	K	L		
495	TCT	NTG	GAC	AAA	GTC	TTC	CGG	GAA	CGG	CGG	GAG	TCC	CTG	AAT	GCC	AGC	ATT	GTG	540
S	X	D	K	V	F	R	E	R	E	R	E	S	L	N	A	S	I	V	D
549	GCC	ATC	AAC	CAA	GCT	GCT	GAC	TGC	TGG	GGT	ATC	CGC	CTN	CGT	TAT	GAG	TAT		594
A	I	N	Q	A	A	D	C	W	G	I	R	C	L	R	Y	E	I		
603	AAG	GAT	ATC	CAT	GTG	CCA	CCC	CGG	GTG	AAA	GAG	TCT	ATG	CAG	ATG	CAG	GTG	GAG	648
K	D	I	H	V	P	P	R	V	K	E	S	M	Q	M	Q	V	E		
657	GCA	GAG	CGG	CGG	AAA	CGG	GCC	ACA	GTT	CTA	GAG	TCT	GAG	GGG	ACC	CGA	GAG	TCG	702
A	E	R	R	K	R	A	T	V	L	E	S	E	G	T	R	E	S		
711	GCC	ATC	AAT	GTG	GCA	GAA	GGG	AAG	AAA	CAG	GCC	CAG	ATC	CTG	GCC	TCC	GAA	GCA	756
A	I	N	V	A	E	G	K	K	K	Q	A	Q	I	L	A	S	E	A	

FIGURE 1B

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GAA	AAG	GCT	GAA	CAG	ATA	AAT	CAG	GCA	GCA	GGA	GAG	GCC	AGT	GCA	GTT	CTG	GCG	810											
E	K	A	E	Q	I	N	Q	A	A	G	E	A	S	A	V	L	A												
AAG	GCC	AAG	GCT	AAA	GCT	GAA	GCT	ATT	CGA	ATC	CTG	GCT	GCA	GCT	CTG	ACA	CAA	864											
K	A	K	A	K	A	E	A	I	R	I	L	A	A	A	L	T	Q												
819		828		837		846		855		864		873		882		891		900											
CAT	AAT	GGA	GAT	GCA	GCA	GCT	TCA	CTG	ACT	GTG	GCC	GAG	CAG	TAT	GTC	AGC	GCG	918											
H	N	G	G	D	A	A	S	L	T	V	A	E	Q	Y	V	S	A												
927		936		945		954		963		972		TTC	TCC	AAA	CTG	GCC	AAG	972											
F	S	K	L	A	K	D	S	N	T	I	L	L	P	S	N	P	G												
981		990		999		1008		1017		1026		GAT	GTC	ACC	AGC	ATG	GCT	CAG	GGT	TAT	GGA	GCC	CTC	ACC	AAA				
D	V	T	S	M	V	A	Q	A	M	G	V	Y	G	A	L	T	K												
1035		1044		1053		1062		1071		1080		GCC	CCA	GTG	CCA	GGG	ACT	CCA	GAC	TCA	CTC	TCC	AGT	GGG	AGC	AGA	GAT	GTC	
A	P	V	P	G	T	P	D	S	L	S	S	G	S	S	R	D	V	*											
1089		1098		1107		1116		1125		1134		CAG	GGT	ACA	GAT	GCA	AGT	NTT	GAT	GAG	GAA	CTT	GAT	CGA	GTC	AAG	ATG	AGT	
O	G	T	D	A	S	X	D	E	E	L	D	R	V	K	M	S	*												

## FIGURE 1C

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1143 TGG AGC TGG GCT TNG CCA GGG AGT CTG GGG ACA AGG AAG CAG ATT TTC CTG ATT  
1152 1161 1170 1179 1188

FIGURE 2A

148	R	--	E R E S L N A S I V D A I N Q A A D C W G I R C L R Y E I K D I H V P P R	789094
165	S	--	D R E E I A H N M Q S T L D D A T D A W G I K V E R V E I K D V K L P V Q	GI 31069
170	S	--	D R E T I A A S M Q T I L D E A T E S W G I K V E R V E I K D V R L P I Q	GI 1065452
197	S	S Q D R R I I S A N L K D E L G S F T C Q F G V E I T D V E I S D V K I -	- GI 1353669	
136	T	--	S R D Q I N A Q L R G V L D E A T G R W G L R V A R V E L R S I D P P P S	Z79701
134	N	--	K R E Y I N S K L L E I L D R E T D A W G V R I E K V E V K E I D P F E D	GI 1591514
186	V K E S M O	M O V E A E R R K R A T V L E S E G T R E S A I N V A E G K K Q A Q	789094	
203	L Q R A M	A A E A A S R E A R A K V I A A E G E M N A - - - - -	GI 31069	
208	L Q R A M	A A E A A T R E A R A K V I A A E G E Q K A - - - - -	GI 1065452	
234	V K E G E N	M G M S A - - - - -	- L S S V A K S D A G Q Q L W Q	GI 1353669
174	I Q A S M E	K Q M K A D R E K R A M I L T A E G T R E A A I K Q A E G Q K Q A Q	Z79701	
172	I K N A M A	Q Q M K A E R L K R A A I L E A E G E K P E - - - - -	GI 1591514	
226	I L A S E A K A E O I N Q A A G E A S A V I L A K A K A E A I - - - - -	789094		
231	- - - - -	- - - - -	- - - - -	GI 31069
236	- - - - -	- - - - -	- - - - -	GI 1065452
260	V I G P	- - - - - V F E D F A K E C A A E E K A K E N A P L V D L - - - - -	GI 1353669	
214	I L A A E G A K	Q A A I L A A E A D R Q S R M L R A Q G E R A A A Y L Q A Q G Q	Z79701	
259	- R I L A A A L T Q H N G D A A A S I L T V A E Q Y V S A F S K L A K D S N T I L	789094		
244	- - - - -	- - - - - S P A A L Q L R Y L Q T L T I I A E K N S T I	GI 31069	
249	- - - - -	- - - - - S P A A L Q L R Y L Q T L N S V A R E K - - - - -	GI 1065452	
288	S D V P S T S A A G T S T D T P N I P S I D I D H L I S V A S L A M D E H - L V	GI 1353669		
254	A K A I E K T F A A I K A G R P T P E M L A Y Q Y L Q T L P E M A R G D A N K V	Z79701		
298	- - - - -	- L P S N P G D V T S M V A Q A M - - G V Y G A L T K A P V P G T P D	789094	
268	- - - - -	- V F E L P I D M - - - - -	GI 31069	
269	- - - - -	- F D D H L P T - - - - -	GI 1065452	
327	R L I G R V F Q I N C K D I E P - I C I D L K H G S G S A Y K G T S L - - N P D	GI 1353669		
294	W V V P S D F N A A L Q G F T R L L G K P G E D G V F - R F E P S P V E D Q P K	Z79701		

FIGURE 2B

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FIGURE 2C

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Library	Lib Description	Abun	Pct Abun
PROSTUT03	prostate tumor, 67 M, match to PROSNOT05	2	0.0703
COLNNOT05	colon, 40 M, match to COLNCRT01	2	0.0577
TESTNOT03	testis, 37 M	1	0.0557
LIVRNOT02	liver, 32 F	1	0.0515
HUVENOB01	HUVEC endothelial cell line, control	1	0.0418
LVENNOT03	heart, left ventricle, 31 M	1	0.0336
PROSTUT01	prostate tumor, 50 M, match to PROSNOT02	1	0.0309
PANCTUT02	pancreatic tumor, carcinoma, 45 F	1	0.0288
KERANOT01	keratinocytes, neonatal M	1	0.0227
CRBLNOT01	brain, cerebellum, 69 M	1	0.0194
LUNGNOT04	lung, 2 M	1	0.0182
PGANNOT01	paraganglia, 46 M	1	0.0159
BRSTTUT01	breast tumor, 55 F, match to BRSTNOT02	1	0.0150

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FIGURE 3